

JUN 21 2001

1645

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/759,152

DATE: 05/30/2001

TIME: 15:39:54

Input Set : A:\4085-235-27 CIP.ST25.txt

Output Set: C:\CRF3\05302001\I759152.raw

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4 <110> APPLICANT: Palmer, Michelle A.J.
5      Gee, Melissa
6      Tillotson, Bonnie
7      Chang, Xiao-Jia
9 <120> TITLE OF INVENTION: Systems for Sensitive Detection of G-Protein Coupled
10      Receptor and Orphan Receptor Function Using Reporter
11      Enzyme Mutant Complementation
13 <130> FILE REFERENCE: 4085-235-27 CIP
15 <140> CURRENT APPLICATION NUMBER: US 09/759,152
16 <141> CURRENT FILING DATE: 2001-01-16
18 <150> PRIOR APPLICATION NUMBER: US 09/654,499
19 <151> PRIOR FILING DATE: 2000-09-01
21 <150> PRIOR APPLICATION NUMBER: US 60/180,669
22 <151> PRIOR FILING DATE: 2000-02-07
24 <160> NUMBER OF SEQ ID NOS: 9
26 <170> SOFTWARE: PatentIn version 3.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 6700
30 <212> TYPE: DNA
31 <213> ORGANISM: Unknown
33 <220> FEATURE:
34 <223> OTHER INFORMATION: pICAST ALC.
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (1457)..(4486)
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45 tcctgccccg gctcagggcc aagaacagat ggtccccaga tgcggtccag ccctcagcag      180
47 tttctagaga accatcagat gtttccaggg tgccccagg acctgaaatg accctgtgcc      240
49 ttatttgaac taaccaatca gtctcgttct cgcttctgtt cgcgcgcttc tgctccccga      300
51 gctcaataaa agagcccaca acccctcact cggggcgcca gtcctccgat tgactgagtc      360
53 gcccggttac ccgtgtatcc aataaaccct cttgcagttg catccgactt gtggtctcgc      420
55 tgttccttgg gaggtctcc tctgagtgat tgactaccgc tcagcggggg tctttcattt      480
57 gggggctcgt ccgggatcgg gagaccctg cccagggacc accgaccac caccgggagg      540
59 caagctggcc agcaacttat ctgtgtctgt ccgattgtct agtgtctatg actgatttta      600
61 tgcgcctgcg tcggtactag ttagctaact agctctgtat ctggcgacc cgtggtggaa      660
63 ctgacgagtt ctgaacaccc ggccgcaacc ctgggagacg tcccaggacg tttgggggcc      720
65 gtttttgtgg cccgacctga ggaagggagt cgatgtggaa tccgaccccg tcaggatatg      780
67 tggttctggt aggagacgag aacctaaaac agttcccgcg tccgtctgaa tttttgcttt      840
69 cggtttgtaa ccgaagccgc gcgtcttgct tgctgcagca tcgttctgtg ttgtctctgt      900
71 ccgactgtgt ttctgtatct gtctgaaaat tagggccaga ctgttaccac tcccttaagt      960
73 ttgaccttag gtaactggaa agatgtcgag cggctcgtct acaaccagtc ggtagatgtc      1020
75 aagaagagac gttgggttac cttctgctct gcagaatggc caacctttaa cgtcggtatg      1080
77 ccgcgagacg gcacctttaa ccgagacctc atcaccaggg ttaagatcaa ggtcttttca      1140
79 cctggcccgc atggacaccc agaccaggtc ccctacatcg tgacctggga agccttggct      1200
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83	ccatccgccc cgtctctccc ccttgaacct cctcgttcga ccccgccctcg atcctccctt	1320
85	tatccagccc tcaactccttc tctaggcgcc ggccgctcta gccattaat acgactcact	1380
87	atagggcgat tcgaatcagg ccttggcgcg ccggtacctt aattaagcgc aattgggagg	1440
89	tggcggtagc ctcgag atg ggc gtg att acg gat tca ctg gcc gtc gtg gcc	1492
90	Met Gly Val Ile Thr Asp Ser Leu Ala Val Val Ala	
91	1 5 10	
93	cgc acc gat cgc cct tcc caa cag tta cgc agc ctg aat ggc gaa tgg	1540
94	Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp	
95	15 20 25	
97	cgc ttt gcc tgg ttt ccg gca cca gaa gcg gtg ccg gaa agc tgg ctg	1588
98	Arg Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu	
99	30 35 40	
101	gag tgc gat ctt cct gag gcc gat act gtc gtc gtc ccc tca aac tgg	1636
102	Glu Cys Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp	
103	45 50 55 60	
105	cag atg cac ggt tac gat gcg ccc atc tac acc aac gtg acc tat ccc	1684
106	Gln Met His Gly Tyr Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro	
107	65 70 75	
109	att acg gtc aat ccg ccg ttt gtt ccc acg gag aat ccg acg ggt tgt	1732
110	Ile Thr Val Asn Pro Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys	
111	80 85 90	
113	tac tcg ctc aca ttt aat gtt gat gaa agc tgg cta cag gaa ggc cag	1780
114	Tyr Ser Leu Thr Phe Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln	
115	95 100 105	
117	acg cga att att ttt gat ggc gtt aac tcg gcg ttt cat ctg tgg tgc	1828
118	Thr Arg Ile Ile Phe Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys	
119	110 115 120	
121	aac ggg cgc tgg gtc ggt tac ggc cag gac agt cgt ttg ccg tct gaa	1876
122	Asn Gly Arg Trp Val Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu	
123	125 130 135 140	
125	ttt gac ctg agc gca ttt tta cgc gcc gga gaa aac cgc ctc gcg gtg	1924
126	Phe Asp Leu Ser Ala Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val	
127	145 150 155	
129	atg gtg ctg cgc tgg agt gac ggc agt tat ctg gaa gat cag gat atg	1972
130	Met Val Leu Arg Trp Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met	
131	160 165 170	
133	tgg cgg atg agc ggc att ttc cgt gac gtc tcg ttg ctg cat aaa ccg	2020
134	Trp Arg Met Ser Gly Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro	
135	175 180 185	
137	act aca caa atc agc gat ttc cat gtt gcc act cgc ttt aat gat gat	2068
138	Thr Thr Gln Ile Ser Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp	
139	190 195 200	
141	ttc agc cgc gct gta ctg gag gct gaa gtt cag atg tgc ggc gag ttg	2116
142	Phe Ser Arg Ala Val Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu	
143	205 210 215 220	
145	cgt gac tac cta cgg gta aca gtt tct tta tgg cag ggt gaa acg cag	2164
146	Arg Asp Tyr Leu Arg Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln	
147	225 230 235	
149	gtc gcc agc ggc acc gcg cct ttc ggc ggt gaa att atc gat gag cgt	2212

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150	Val	Ala	Ser	Gly	Thr	Ala	Pro	Phe	Gly	Gly	Glu	Ile	Ile	Asp	Glu	Arg	
151				240					245					250			
153	ggt	ggt	tat	gcc	gat	cgc	gtc	aca	cta	cgt	ctg	aac	gtc	gaa	aac	ccg	2260
154	Gly	Gly	Tyr	Ala	Asp	Arg	Val	Thr	Leu	Arg	Leu	Asn	Val	Glu	Asn	Pro	
155			255				260						265				
157	aaa	ctg	tgg	agc	gcc	gaa	atc	ccg	aat	ctc	tat	cgt	gcg	gtg	gtt	gaa	2308
158	Lys	Leu	Trp	Ser	Ala	Glu	Ile	Pro	Asn	Leu	Tyr	Arg	Ala	Val	Val	Glu	
159		270					275					280					
161	ctg	cac	acc	gcc	gac	ggc	acg	ctg	att	gaa	gca	gaa	gcc	tgc	gat	gtc	2356
162	Leu	His	Thr	Ala	Asp	Gly	Thr	Leu	Ile	Glu	Ala	Glu	Ala	Cys	Asp	Val	
163	285					290				295						300	
165	ggt	ttc	cgc	gag	gtg	cgg	att	gaa	aat	ggt	ctg	ctg	ctg	ctg	aac	ggc	2404
166	Gly	Phe	Arg	Glu	Val	Arg	Ile	Glu	Asn	Gly	Leu	Leu	Leu	Leu	Asn	Gly	
167				305					310						315		
169	aag	ccg	ttg	ctg	att	cga	ggc	gtt	aac	cgt	cac	gag	cat	cat	cct	ctg	2452
170	Lys	Pro	Leu	Leu	Ile	Arg	Gly	Val	Asn	Arg	His	Glu	His	His	Pro	Leu	
171			320					325						330			
173	cat	ggt	cag	gtc	atg	gat	gag	cag	acg	atg	gtg	cag	gat	atc	ctg	ctg	2500
174	His	Gly	Gln	Val	Met	Asp	Glu	Gln	Thr	Met	Val	Gln	Asp	Ile	Leu	Leu	
175			335				340					345					
177	atg	aag	cag	aac	aac	ttt	aac	gcc	gtg	cgc	tgt	tcg	cat	tat	ccg	aac	2548
178	Met	Lys	Gln	Asn	Asn	Phe	Asn	Ala	Val	Arg	Cys	Ser	His	Tyr	Pro	Asn	
179		350				355					360						
181	cat	ccg	ctg	tgg	tac	acg	ctg	tgc	gac	cgc	tac	ggc	ctg	tat	gtg	gtg	2596
182	His	Pro	Leu	Trp	Tyr	Thr	Leu	Cys	Asp	Arg	Tyr	Gly	Leu	Tyr	Val	Val	
183	365					370				375					380		
185	gat	gaa	gcc	aat	att	gaa	acc	cac	ggc	atg	gtg	cca	atg	aat	cgt	ctg	2644
186	Asp	Glu	Ala	Asn	Ile	Glu	Thr	His	Gly	Met	Val	Pro	Met	Asn	Arg	Leu	
187				385					390					395			
189	acc	gat	gat	ccg	cgc	tgg	cta	ccg	gcg	atg	agc	gaa	cgc	gta	acg	cga	2692
190	Thr	Asp	Asp	Pro	Arg	Trp	Leu	Pro	Ala	Met	Ser	Glu	Arg	Val	Thr	Arg	
191			400					405						410			
193	atg	gtg	cag	cgc	gat	cgt	aat	cac	ccg	agt	gtg	atc	atc	tgg	tcg	ctg	2740
194	Met	Val	Gln	Arg	Asp	Arg	Asn	His	Pro	Ser	Val	Ile	Ile	Trp	Ser	Leu	
195			415				420					425					
197	ggg	aat	gaa	tca	ggc	cac	ggc	gct	aat	cac	gac	gcg	ctg	tat	cgc	tgg	2788
198	Gly	Asn	Glu	Ser	Gly	His	Gly	Ala	Asn	His	Asp	Ala	Leu	Tyr	Arg	Trp	
199		430				435					440						
201	atc	aaa	tct	gtc	gat	cct	tcc	cgc	ccg	gtg	cag	tat	gaa	ggc	ggc	gga	2836
202	Ile	Lys	Ser	Val	Asp	Pro	Ser	Arg	Pro	Val	Gln	Tyr	Glu	Gly	Gly	Gly	
203	445					450				455					460		
205	gcc	gac	acc	acg	gcc	acc	gat	att	att	tgc	ccg	atg	tac	gcg	cgc	gtg	2884
206	Ala	Asp	Thr	Thr	Ala	Thr	Asp	Ile	Ile	Cys	Pro	Met	Tyr	Ala	Arg	Val	
207				465					470				475				
209	gat	gaa	gac	cag	ccc	ttc	ccg	gct	gtg	ccg	aaa	tgg	tcc	atc	aaa	aaa	2932
210	Asp	Glu	Asp	Gln	Pro	Phe	Pro	Ala	Val	Pro	Lys	Trp	Ser	Ile	Lys	Lys	
211			480					485					490				
213	tgg	ctt	tcg	cta	cct	gga	gag	acg	cgc	ccg	ctg	atc	ctt	tgc	gaa	tac	2980
214	Trp	Leu	Ser	Leu	Pro	Gly	Glu	Thr	Arg	Pro	Leu	Ile	Leu	Cys	Glu	Tyr	

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217 gcc cac gcg atg ggt aac agt ctt ggc ggt ttc gct aaa tac tgg cag				3028
218 Ala His Ala Met Gly Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln				
219 510	515	520		
221 gcg ttt cgt cag tat ccc cgt tta cag ggc ggc ttc gtc tgg gac tgg				3076
222 Ala Phe Arg Gln Tyr Pro Arg Leu Gln Gly Gly Phe Val Trp Asp Trp				
223 525	530	535	540	
225 gtg gat cag tcg ctg att aaa tat gat gaa aac ggc aac ccg tgg tcg				3124
226 Val Asp Gln Ser Leu Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser				
227 545	550	555		
229 gct tac ggc ggt gat ttt ggc gat acg ccg aac gat cgc cag ttc tgt				3172
230 Ala Tyr Gly Gly Asp Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys				
231 560	565	570		
233 atg aac ggt ctg gtc ttt gcc gac cgc acg ccg cat cca gcg ctg acg				3220
234 Met Asn Gly Leu Val Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr				
235 575	580	585		
237 gaa gca aaa cac cag cag cag ttt ttc cag ttc cgt tta tcc ggg caa				3268
238 Glu Ala Lys His Gln Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Gln				
239 590	595	600		
241 acc atc gaa gtg acc agc gaa tac ctg ttc cgt cat agc gat aac gag				3316
242 Thr Ile Glu Val Thr Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu				
243 605	610	615	620	
245 ctc ctg cac tgg atg gtg gcg ctg gat ggt aag ccg ctg gca agc ggt				3364
246 Leu Leu His Trp Met Val Ala Leu Asp Gly Lys Pro Leu Ala Ser Gly				
247 625	630	635		
249 gaa gtg cct ctg gat gtc gct cca caa ggt aaa cag ttg att gaa ctg				3412
250 Glu Val Pro Leu Asp Val Ala Pro Gln Gly Lys Gln Leu Ile Glu Leu				
251 640	645	650		
253 cct gaa cta ccg cag ccg gag agc gcc ggg caa ctc tgg ctc aca gta				3460
254 Pro Glu Leu Pro Gln Pro Glu Ser Ala Gly Gln Leu Trp Leu Thr Val				
255 655	660	665		
257 cgc gta gtg caa ccg aac gcg acc gca tgg tca gaa gcc ggg cac atc				3508
258 Arg Val Val Gln Pro Asn Ala Thr Ala Trp Ser Glu Ala Gly His Ile				
259 670	675	680		
261 agc gcc tgg cag cag tgg cgt ctg gcg gaa aac ctc agt gtg acg ctc				3556
262 Ser Ala Trp Gln Gln Trp Arg Leu Ala Glu Asn Leu Ser Val Thr Leu				
263 685	690	695	700	
265 ccc gcc gcg tcc cac gcc atc ccg cat ctg acc acc agc gaa atg gat				3604
266 Pro Ala Ala Ser His Ala Ile Pro His Leu Thr Thr Ser Glu Met Asp				
267 705	710	715		
269 ttt tgc atc gag ctg ggt aat aag cgt tgg caa ttt aac cgc cag tca				3652
270 Phe Cys Ile Glu Leu Gly Asn Lys Arg Trp Gln Phe Asn Arg Gln Ser				
271 720	725	730		
273 ggc ttt ctt tca cag atg tgg att ggc gat aaa aaa caa ctg ctg acg				3700
274 Gly Phe Leu Ser Gln Met Trp Ile Gly Asp Lys Lys Gln Leu Leu Thr				
275 735	740	745		
277 ccg ctg cgc gat cag ttc acc cgt gca ccg ctg gat aac gac att ggc				3748
278 Pro Leu Arg Asp Gln Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly				
279 750	755	760		

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281	gta agt gaa gcg acc cgc att gac cct aac gcc tgg gtc gaa cgc tgg	3796
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283	765 770 775 780	
285	aag gcg gcg ggc cat tac cag gcc gaa gca gcg ttg ttg cag tgc acg	3844
286	Lys Ala Ala Gly His Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr	
287	785 790 795	
289	gca gat aca ctt gct gat gcg gtg ctg att acg acc gct cac gcg tgg	3892
290	Ala Asp Thr Leu Ala Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp	
291	800 805 810	
293	cag cat cag ggg aaa acc tta ttt atc agc cgg aaa acc tac cgg att	3940
294	Gln His Gln Gly Lys Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile	
295	815 820 825	
297	gat ggt agt ggt caa atg gcg att acc gtt gat gtt gaa gtg gcg agc	3988
298	Asp Gly Ser Gly Gln Met Ala Ile Thr Val Asp Val Glu Val Ala Ser	
299	830 835 840	
301	gat aca ccg cat ccg gcg cgg att ggc ctg aac tgc cag ctg gcg cag	4036
302	Asp Thr Pro His Pro Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln	
303	845 850 855 860	
305	gta gca gag cgg gta aac tgg ctc gga tta ggg ccg caa gaa aac tat	4084
306	Val Ala Glu Arg Val Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr	
307	865 870 875	
309	ccc gac cgc ctt act gcc gcc tgt ttt gac cgc tgg gat ctg cca ttg	4132
310	Pro Asp Arg Leu Thr Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu	
311	880 885 890	
313	tca gac atg tat acc ccg tac gtc ttc ccg agc gaa aac ggt ctg cgc	4180
314	Ser Asp Met Tyr Thr Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg	
315	895 900 905	
317	tgc ggg acg cgc gaa ttg aat tat ggc cca cac cag tgg cgc ggc gac	4228
318	Cys Gly Thr Arg Glu Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp	
319	910 915 920	
321	ttc cag ttc aac atc agc cgc tac agt caa cag caa ctg atg gaa acc	4276
322	Phe Gln Phe Asn Ile Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr	
323	925 930 935 940	
325	agc cat cgc cat ctg ctg cac gcg gaa gaa ggc aca tgg ctg aat atc	4324
326	Ser His Arg His Leu Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile	
327	945 950 955	
329	gac ggt ttc cat atg ggg att ggt ggc gac gac tcc tgg agc ccg tca	4372
330	Asp Gly Phe His Met Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser	
331	960 965 970	
333	gta tcg gcg gaa ttc cag ctg agc gcc ggt cgc tac cat tac cag ttg	4420
334	Val Ser Ala Glu Phe Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu	
335	975 980 985	
337	gtc tgg tgt caa aaa aga tct gac tat aaa gat gag gac ctc gac cat	4468
338	Val Trp Cys Gln Lys Arg Ser Asp Tyr Lys Asp Glu Asp Leu Asp His	
339	990 995 1000	
341	cat cat cat cat cac cgg taataatagg tagataagtg actgattaga	4516
342	His His His His His Arg	
343	1005 1010	
345	tgcattgatc cctcgaccaa ttccggttat tttccaccat attgccgtct tttggcaatg	4576

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